



## SEQUENCE LISTING

&lt;110&gt; BJORN, Sara et al

&lt;120&gt; NOVEL FLUORESCENT PROTEINS

&lt;130&gt; 3759-0115P

&lt;140&gt; US 09/887,784

&lt;141&gt; 2001-06-19

&lt;160&gt; 24

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 720

&lt;212&gt; DNA

&lt;213&gt; Aequoria Victoria

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(717)

&lt;400&gt; 1

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1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35					40					45			
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	aca	cta	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	tct	tac	ggc	gtg	cag	tgc	ttc	agc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cag	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120						125			

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
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 130 135 140  
  
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 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
  
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
 165 170 175  
  
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
  
 ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
 195 200 205  
  
 agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
 210 215 220  
  
 gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 717  
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 225 230 235  
  
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 35 40 45  
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190  
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
225 230 235

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<220>  
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<222> (1)...(717)

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc aca cta gtg acc acc 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ctg tct tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240  
Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288  
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95  
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110  
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384  
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125  
atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac 432  
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

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145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc	576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg	624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	
195 200 205	
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctc cta ggg ttc	672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe	
210 215 220	
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	717
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225 230 235	
taa	720

<210> 4  
 <211> 239  
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 <213> Aequoria Victoria

<400> 4

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20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	
180 185 190	
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu	

195                      200                      205  
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe  
 210                      215                      220  
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 225                      230                      235

<210> 5  
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<220>  
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 <222> (1)...(714)

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 gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt gga gag 96  
 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu  
 20                      25                      30  
  
 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc 144  
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35                      40                      45  
  
 act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc 192  
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu  
 50                      55                      60  
  
 tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag 240  
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65                      70                      75                      80  
  
 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga 288  
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85                      90                      95  
  
 act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc 336  
 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100                      105                      110  
  
 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att 384  
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115                      120                      125  
  
 gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat 432  
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn  
 130                      135                      140  
  
 tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc 480  
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly  
 145                      150                      155                      160  
  
 atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga agc gtt 528

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val	
165 170 175	
caa tta gca gac cat tat caa caa aat act cca att ggc gat ggc cct	576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
180 185 190	
gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc ctt tcc	624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
195 200 205	
aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta	672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val	
210 215 220	
aca gct gct ggg att aca cat ggc atg gat gaa ggg tac aag	714
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Gly Tyr Lys	
225 230 235	
taa	717
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn	
130 135 140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly	
145 150 155 160	
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val	
165 170 175	
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	
180 185 190	
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser	
195 200 205	
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val	
210 215 220	
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Gly Tyr Lys	
225 230 235	

<210> 7  
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 <212> DNA  
 <213> Aequovia Victoria

<220>  
 <221> CDS  
 <222> (1)...(717)

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 gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt gga gag	96
Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu	
20 25 30	
 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
 act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
 tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag	240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln	
65 70 75 80	
 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
 act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc	336
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
 gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn	
130 135 140	
 tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly	
145 150 155 160	
 atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga agc gtt	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val	
165 170 175	
 caa tta gca gac cat tat caa caa aat act cca att ggc gat ggc cct	576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	

180	185	190	
gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc ctt tcc			624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
195	200	205	
aaa gat ccc aac gaa aag aga gat cac atg atc ctc cta ggg ttt gta			672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Gly Phe Val			
210	215	220	
aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa taa			717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys *			
225	230	235	

<210> 8  
 <211> 238  
 <212> PRT  
 <213> Aequovia Victoria

<400> 8

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
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Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85	90	95	
Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105	110	
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
115	120	125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn			
130	135	140	
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly			
145	150	155	160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val			
165	170	175	
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
180	185	190	
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
195	200	205	
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Gly Phe Val			
210	215	220	
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys			
225	230	235	

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 <210> 14

<211> 29  
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 ttattgtac cttcatcca tgccatgtg 29  
  
  
 <210> 15  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR Primer  
  
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 <211> 41  
 <212> DNA  
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 <223> PCR Primer  
  
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 <400> 17  
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 <210> 18  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> PCR Primer  
  
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 gaacaccata agaaaacggt gtgacaagcg ttgg 34

<210> 19  
<211> 34  
<212> DNA  
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<220>  
<223> PCR Primer

<400> 19  
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34

<210> 20  
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<212> DNA  
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<220>  
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34

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<220>  
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<400> 21  
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32

<210> 22  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 22  
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31

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<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR Primer

<400> 23  
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32

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<213> Artificial Sequence

<220>  
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31